

SEQUENCE LISTING

<110> Reindl, Andreas  
Mejia, Patricia Leon  
Palmas, Juan Manual Esteves  
Gracia, Maria Araceli Cantero  
Ebneth, Marcus  
Herbers, Karin

<120> DNA sequence coding for a 1-deoxy-D-xylulose-5-phosphate synthase and overproduction thereof in plants

<130> 0817/000006/MEC

<140> US 09/762,045

<141> 2001-02-01

<150> PCT/EP99/05467

<151> 1999-07-30

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<170> PatentIn Vers. 2.0/WordPerfect 6.0

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Gln	Ala	Tyr	Pro	His	Lys	Ile	Leu	Thr	Gly	Arg	Arg	Asp	Lys	Ile	Gly	
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Thr	Ile	Arg	Gln	Lys	Gly	Gly	Leu	His	Pro	Phe	Pro	Trp	Arg	Gly	Glu	
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Ser	Glu	Tyr	Asp	Val	Leu	Ser	Val	Gly	His	Ser	Ser	Thr	Ser	Ile	Ser	
		115					120					125				
Ala	Gly	Ile	Gly	Ile	Ala	Val	Ala	Ala	Glu	Lys	Glu	Gly	Lys	Asn	Arg	
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Phe	Glu	Ala	Met	Asn	His	Ala	Gly	Asp	Ile	Arg	Pro	Asp	Met	Leu	Val	
				165					170					175		
Ile	Leu	Asn	Asp	Asn	Glu	Met	Ser	Ile	Ser	Glu	Asn	Val	Gly	Ala	Leu	
		180						185					190			
Asn	Asn	His	Leu	Ala	Gln	Leu	Leu	Ser	Gly	Lys	Leu	Tyr	Ser	Ser	Leu	
		195					200					205				
Arg	Glu	Gly	Gly	Lys	Lys	Val	Phe	Ser	Gly	Val	Pro	Pro	Ile	Lys	Glu	
	210					215					220					

Leu Leu Lys Arg Thr Glu Glu His Ile Lys Gly Met Val Val Pro Gly  
 225 230 235 240  
 Thr Leu Phe Glu Glu Leu Gly Phe Asn Tyr Ile Gly Pro Val Asp Gly  
 245 250 255  
 His Asp Val Leu Gly Leu Ile Thr Thr Leu Lys Asn Met Arg Asp Leu  
 260 265 270  
 Lys Gly Pro Gln Phe Leu His Ile Met Thr Lys Lys Gly Arg Gly Tyr  
 275 280 285  
 Glu Pro Ala Glu Lys Asp Pro Ile Thr Phe His Ala Val Pro Lys Phe  
 290 295 300  
 Asp Pro Ser Ser Gly Cys Leu Pro Lys Ser Ser Gly Gly Leu Pro Ser  
 305 310 315 320  
 Tyr Ser Lys Ile Phe Gly Asp Trp Leu Cys Glu Thr Ala Ala Lys Asp  
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 Asn Lys Leu Met Ala Ile Thr Pro Ala Met Arg Glu Gly Ser Gly Met  
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 Val Glu Phe Ser Arg Lys Phe Pro Asp Arg Tyr Phe Asp Val Ala Ile  
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 Tyr Lys Pro Ile Val Ala Ile Tyr Ser Thr Phe Leu Gln Arg Ala Tyr  
 385 390 395 400  
 Asp Gln Val Leu His Asp Val Ala Ile Gln Lys Leu Pro Val Leu Phe  
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 Ala Ile Asp Arg Ala Gly Ile Val Gly Ala Asp Gly Gln Thr His Gln  
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 Gly Ala Phe Asp Leu Ser Tyr Leu Arg Cys Ile Pro Glu Met Val Ile  
 435 440 445  
 Met Thr Pro Ser Asp Glu Asn Glu Cys Arg Gln Met Leu Tyr Thr Gly  
 450 455 460  
 Tyr His Tyr Asn Asp Gly Pro Ser Ala Val Arg Tyr Pro Arg Gly Asn  
 465 470 475 480  
 Ala Val Gly Val Glu Leu Thr Pro Leu Glu Lys Leu Pro Ile Gly Lys  
 485 490 495  
 Gly Ile Val Lys Arg Arg Gly Glu Lys Leu Ala Ile Leu Asn Phe Gly  
 500 505 510  
 Thr Leu Met Pro Glu Ala Ala Lys Val Ala Glu Ser Leu Asn Ala Thr  
 515 520 525  
 Leu Val Asp Met Arg Phe Val Lys Pro Leu Asp Glu Ala Leu Ile Leu

530		535		540
Glu Met Ala Ala Ser His Glu Ala Leu Val Thr Val Glu Glu Asn Ala				
545		550		560
Ile Met Gly Gly Ala Gly Ser Gly Val Asn Glu Val Leu Met Ala His				
	565		570	575
Arg Lys Pro Val Pro Val Leu Asn Ile Gly Leu Pro Asp Phe Phe Ile				
	580		585	590
Pro Gln Gly Thr Gln Glu Glu Met Arg Ala Glu Leu Gly Leu Asp Ala				
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Ala Gly Met Glu Ala Lys Ile Lys Ala Trp Leu Ala				
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 <212> DNA  
 <213> Streptomyces avermitilis

<220>  
 <221> CDS  
 <222> (218)..(1138)

<400> 5

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gagcactccg atgcgcggct cccgcgccag cagcaccagg agccggccgt ccagatgac	180
gatcgccacg gcagcccctc cagtgggtcat cctgtac atg cag ccc cac gcc atg	235
	Met Gln Pro His Ala Met
	1 5
ggc ggt gca ctg aac aca ttg tcc agc gga caa gcc aac tat tgc gca	283
Gly Gly Ala Leu Asn Thr Leu Ser Ser Gly Gln Ala Asn Tyr Cys Ala	
	10 15 20
cct tgc gga acg gag cga ccc tgc cgc cat gac gca gac cac aca cca	331
Pro Cys Gly Thr Glu Arg Pro Cys Arg His Asp Ala Asp His Thr Pro	
	25 30 35
cac tcc cga cac cgc ccg gca ggc cga ccc ctt ccc ggt gaa ggg aat	379
His Ser Arg His Arg Pro Ala Gly Arg Pro Leu Pro Gly Glu Gly Asn	
	40 45 50
gga cgc ggt cgt ctt cgc cgt agg caa cgc caa gca ggc cgc gca cta	427
Gly Arg Gly Arg Leu Arg Arg Arg Gln Arg Gln Ala Gly Arg Ala Leu	
	55 60 65 70
ctc cac cgc ctt cgg cat gca gct tgt ggc gta ctc cgg acc gga gaa	475
Leu His Arg Leu Arg His Ala Ala Cys Gly Val Leu Arg Thr Gly Glu	
	75 80 85

cgg cag ccg cga gac cgc ttc gta cgt cct cac caa cgg ctc ggc acg Arg Gln Pro Arg Asp Arg Phe Val Arg Pro His Gln Arg Leu Gly Thr 90 95 100	523
ctt cgt cct cac ctc cgt cat caa gcc cgc cac ccc ctg ggg cca ctt Leu Arg Pro His Leu Arg His Gln Ala Arg His Pro Leu Gly Pro Leu 105 110 115	571
cct cgc cga cca tgt ggc cga gca cgg cga cgg cgt cgt cga cct cgc Pro Arg Arg Pro Cys Gly Arg Ala Arg Arg Arg Arg Arg Pro Arg 120 125 130	619
cat cga ggt ccc gga cgc ccg cgc cgc cca cgc gta cgc gat cga gca His Arg Gly Pro Gly Arg Pro Arg Arg Pro Arg Val Arg Asp Arg Ala 135 140 145 150	667
cgg cgc ccg ctc ggt cgc cga gcc gta cga gct gaa gga cga gca cgg Arg Arg Pro Leu Gly Arg Arg Ala Val Arg Ala Glu Gly Arg Ala Arg 155 160 165	715
cac ggt cgt cct cgc cgc gat cgc cac cta cgg caa gac ccg cca cac His Gly Arg Pro Arg Arg Asp Arg His Leu Arg Gln Asp Pro Pro His 170 175 180	763
cct cgt cga ccg gac cgg cta cga cgg ccc cta cct ccc cgg cta cgt Pro Arg Arg Pro Asp Arg Leu Arg Arg Pro Leu Pro Pro Arg Leu Arg 185 190 195	811
ggc cgc cgc ccc gat cgt cga acc gcc cgc cca ccg cac ctt cca ggc Gly Arg Arg Pro Asp Arg Arg Thr Ala Arg Pro Pro His Leu Pro Gly 200 205 210	859
cat cga cca ctg cgt cgg caa cgt cga gct cgg ccg gat gaa cga atg His Arg Pro Leu Arg Arg Gln Arg Arg Ala Arg Pro Asp Glu Arg Met 215 220 225 230	907
ggt cgg ctt cta caa caa ggt cat ggg ctt cac gaa cat gaa gga gtt Gly Arg Leu Leu Gln Gln Gly His Gly Leu His Glu His Glu Gly Val 235 240 245	955
cgt ggg cga cga cat cgc gac cga gta ctc ggc gct gat gtc gaa ggt Arg Gly Arg Arg His Arg Asp Arg Val Leu Gly Ala Asp Val Glu Gly 250 255 260	1003
cgt ggc cga cgg cac gct caa ggt caa gtt ccc gat caa cga gcc cgc Arg Gly Arg Arg His Ala Gln Gly Gln Val Pro Asp Gln Arg Ala Arg 265 270 275	1051
cct cgc caa gaa gaa gtc cca gat cga cga gta cct gga gtt cta cgg Pro Arg Gln Glu Glu Val Pro Asp Arg Arg Val Pro Gly Val Leu Arg 280 285 290	1099
cgg cgc ggg cgt cca gca cat cgc gct gaa cac ggg tga catcgtcgag Arg Arg Gly Arg Pro Ala His Arg Ala Glu His Gly 295 300 305	1148
acggtacgca cgatgcgcgc cgccggcgtc cagttcctgg acacgcccg ctcgtactac	1208
gacaccctcg gggagtgggt gggcgacacc cgcgtccccg tcgacaccct gcgcgagctg	1268

aagatcctcg cggaccgcga cgaggacggc tatctgctcc agatcttcac caagccggtc 1328  
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<210> 6

<211> 306

<212> PRT

<213> *Streptomyces avermitilis*

<400> 6

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Asp	Ala	Asp	His	Thr	Pro	His	Ser	Arg	His	Arg	Pro	Ala	Gly	Arg	Pro	35	40	45	
Leu	Pro	Gly	Glu	Gly	Asn	Gly	Arg	Gly	Arg	Leu	Arg	Arg	Arg	Gln	Arg	50	55	60	
Gln	Ala	Gly	Arg	Ala	Leu	Leu	His	Arg	Leu	Arg	His	Ala	Ala	Cys	Gly	65	70	75	80
Val	Leu	Arg	Thr	Gly	Glu	Arg	Gln	Pro	Arg	Asp	Arg	Phe	Val	Arg	Pro	85	90	95	
His	Gln	Arg	Leu	Gly	Thr	Leu	Arg	Pro	His	Leu	Arg	His	Gln	Ala	Arg	100	105	110	
His	Pro	Leu	Gly	Pro	Leu	Pro	Arg	Pro	Cys	Gly	Arg	Ala	Arg	Arg	115	120	125		
Arg	Arg	Arg	Arg	Pro	Arg	His	Arg	Gly	Pro	Gly	Arg	Pro	Arg	Arg	Pro	130	135	140	
Arg	Val	Arg	Asp	Arg	Ala	Arg	Arg	Pro	Leu	Gly	Arg	Arg	Ala	Val	Arg	145	150	155	160
Ala	Glu	Gly	Arg	Ala	Arg	His	Gly	Arg	Pro	Arg	Arg	Asp	Arg	His	Leu	165	170	175	
Arg	Gln	Asp	Pro	Pro	His	Pro	Arg	Arg	Pro	Asp	Arg	Leu	Arg	Arg	Pro	180	185	190	
Leu	Pro	Pro	Arg	Leu	Arg	Gly	Arg	Arg	Pro	Asp	Arg	Arg	Thr	Ala	Arg	195	200	205	
Pro	Pro	His	Leu	Pro	Gly	His	Arg	Pro	Leu	Arg	Arg	Gln	Arg	Arg	Ala	210	215	220	

Arg Pro Asp Glu Arg Met Gly Arg Leu Leu Gln Gln Gly His Gly Leu  
 225 230 235 240  
 His Glu His Glu Gly Val Arg Gly Arg Arg His Arg Asp Arg Val Leu  
 245 250 255  
 Gly Ala Asp Val Glu Gly Arg Gly Arg Arg His Ala Gln Gly Gln Val  
 260 265 270  
 Pro Asp Gln Arg Ala Arg Pro Arg Gln Glu Glu Val Pro Asp Arg Arg  
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<210> 7  
 <211> 1479  
 <212> DNA  
 <213> Arabidopsis thaliana

<220>  
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 <222> (1)..(1401)

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Ser Thr Glu Gln Thr Asn Phe Val Ser His Val Pro Ser Ser Leu Ser	
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ctc cct caa cga cgg acc tct ctc cga gta acc gca gcc agg gcc act	144
Leu Pro Gln Arg Arg Thr Ser Leu Arg Val Thr Ala Ala Arg Ala Thr	
35 40 45	
ccc aaa ctc tcc aac cgt aaa ctc cgt gtc gcc gtc atc ggt ggt gga	192
Pro Lys Leu Ser Asn Arg Lys Leu Arg Val Ala Val Ile Gly Gly Gly	
50 55 60	
cca gca ggc ggg gca gct gca gag act cta gca caa gga gga atc gag	240
Pro Ala Gly Gly Ala Ala Ala Glu Thr Leu Ala Gln Gly Gly Ile Glu	
65 70 75 80	
acg att ctc atc gag cgt aag atg gac aat tgc aag cct tgc ggt ggc	288
Thr Ile Leu Ile Glu Arg Lys Met Asp Asn Cys Lys Pro Cys Gly Gly	
85 90 95	
gcg att cct ctc tgt atg gtc gga gaa ttc aac ttg ccg ttg gat att	336
Ala Ile Pro Leu Cys Met Val Gly Glu Phe Asn Leu Pro Leu Asp Ile	
100 105 110	
att gat cgg aga gtg acg aag atg aag atg att tcg ccg tcg aac att	384

Ile	Asp	Arg	Arg	Val	Thr	Lys	Met	Lys	Met	Ile	Ser	Pro	Ser	Asn	Ile		
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gct	ggt	gat	att	ggg	cgt	acg	ctt	aag	gag	cat	gag	tat	ata	ggg	atg	432	
Ala	Val	Asp	Ile	Gly	Arg	Thr	Leu	Lys	Glu	His	Glu	Tyr	Ile	Gly	Met		
	130					135					140						
gtg	aga	aga	gaa	ggt	ctt	gat	gct	tat	ctg	aga	gag	aga	gct	gag	aag	480	
Val	Arg	Arg	Glu	Val	Leu	Asp	Ala	Tyr	Leu	Arg	Glu	Arg	Ala	Glu	Lys		
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agt	gga	gcc	act	gtg	att	aac	ggg	ctc	ttc	ctt	aag	atg	gat	cat	ccg	528	
Ser	Gly	Ala	Thr	Val	Ile	Asn	Gly	Leu	Phe	Leu	Lys	Met	Asp	His	Pro		
				165					170					175			
gag	aat	tgg	gac	tcg	ccg	tac	act	ttg	cat	tac	act	gag	tac	gat	ggg	576	
Glu	Asn	Trp	Asp	Ser	Pro	Tyr	Thr	Leu	His	Tyr	Thr	Glu	Tyr	Asp	Gly		
			180					185					190				
aaa	act	gga	gct	aca	ggg	acg	aag	aaa	aca	atg	gag	ggt	gat	gct	gtc	624	
Lys	Thr	Gly	Ala	Thr	Gly	Thr	Lys	Lys	Thr	Met	Glu	Val	Asp	Ala	Val		
	195						200					205					
att	gga	gct	gat	gga	gct	aac	tct	agg	ggt	gct	aaa	tct	att	gat	gct	672	
Ile	Gly	Ala	Asp	Gly	Ala	Asn	Ser	Arg	Val	Ala	Lys	Ser	Ile	Asp	Ala		
	210					215					220						
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Gly	Asp	Tyr	Asp	Tyr	Ala	Ile	Ala	Phe	Gln	Glu	Arg	Ile	Arg	Ile	Pro		
225					230				235						240		
gat	gag	aaa	atg	act	tac	tat	gag	gat	tta	gct	gag	atg	tat	ggt	gga	768	
Asp	Glu	Lys	Met	Thr	Tyr	Tyr	Glu	Asp	Leu	Ala	Glu	Met	Tyr	Val	Gly		
				245					250					255			
gat	gat	gtg	tcg	ccg	gat	ttc	tat	ggg	tgg	gtg	ttc	cct	aag	tgc	gac	816	
Asp	Asp	Val	Ser	Pro	Asp	Phe	Tyr	Gly	Trp	Val	Phe	Pro	Lys	Cys	Asp		
		260						265					270				
cat	gta	gct	ggt	gga	aca	ggg	act	gtg	act	cac	aaa	ggg	gac	atc	aag	864	
His	Val	Ala	Val	Gly	Thr	Gly	Thr	Val	Thr	His	Lys	Gly	Asp	Ile	Lys		
	275						280					285					
aag	ttc	cag	ctc	gcg	acc	aga	aac	aga	gct	aag	gac	aag	att	ctt	gga	912	
Lys	Phe	Gln	Leu	Ala	Thr	Arg	Asn	Arg	Ala	Lys	Asp	Lys	Ile	Leu	Gly		
	290					295					300						
ggg	aag	atc	atc	cgt	gtg	gag	gct	cat	ccg	att	cct	gaa	cat	ccg	aga	960	
Gly	Lys	Ile	Ile	Arg	Val	Glu	Ala	His	Pro	Ile	Pro	Glu	His	Pro	Arg		
305					310				315						320		
cca	cgt	agg	ctc	tcg	aaa	cgt	gtg	gct	ctt	gta	ggg	gat	gct	gca	ggg	1008	
Pro	Arg	Arg	Leu	Ser	Lys	Arg	Val	Ala	Leu	Val	Gly	Asp	Ala	Ala	Gly		
				325					330					335			
tat	gtg	act	aaa	tgc	tct	ggg	gaa	ggg	atc	tac	ttt	gct	gct	aag	agt	1056	
Tyr	Val	Thr	Lys	Cys	Ser	Gly	Glu	Gly	Ile	Tyr	Phe	Ala	Ala	Lys	Ser		
			340					345					350				



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 Gly Arg Met Cys Ala Glu Ala Ile Val Glu Gly Ser Gln Asn Gly Lys  
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 Lys Met Ile Asp Glu Gly Asp Leu Arg Lys Tyr Leu Glu Lys Trp Asp  
 370 375 380  
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 Lys Thr Tyr Leu Pro Thr Tyr Arg Val Leu Asp Val Leu Gln Lys Val  
 385 390 395 400  
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 Phe Tyr Arg Ser Asn Pro Ala Arg Glu Ala Phe Val Glu Met Cys Asn  
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 Asp Glu Tyr Val Gln Lys Met Thr Phe Asp Ser Tyr Leu Tyr Lys Arg  
 420 425 430  
 gtt gcg ccg ggt agt cct ttg gag gat atc aag ttg gct gtg aac acc 1344  
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 Ile Gly Ser Leu Val Arg Ala Asn Ala Leu Arg Arg Glu Ile Glu Lys  
 450 455 460  
 ctt agt gtt taagaaacaa ataatgaggt ctatctcctt tcttcatctc 1441  
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 <212> PRT  
 <213> Arabidopsis thaliana

<400> 8

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 35 40 45  
 Pro Lys Leu Ser Asn Arg Lys Leu Arg Val Ala Val Ile Gly Gly Gly  
 50 55 60  
 Pro Ala Gly Gly Ala Ala Ala Glu Thr Leu Ala Gln Gly Gly Ile Glu  
 65 70 75 80  
 Thr Ile Leu Ile Glu Arg Lys Met Asp Asn Cys Lys Pro Cys Gly Gly

85										90					95				
Ala	Ile	Pro	Leu	Cys	Met	Val	Gly	Glu	Phe	Asn	Leu	Pro	Leu	Asp	Ile				
			100					105					110						
Ile	Asp	Arg	Arg	Val	Thr	Lys	Met	Lys	Met	Ile	Ser	Pro	Ser	Asn	Ile				
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Ala	Val	Asp	Ile	Gly	Arg	Thr	Leu	Lys	Glu	His	Glu	Tyr	Ile	Gly	Met				
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Val	Arg	Arg	Glu	Val	Leu	Asp	Ala	Tyr	Leu	Arg	Glu	Arg	Ala	Glu	Lys				
145					150					155					160				
Ser	Gly	Ala	Thr	Val	Ile	Asn	Gly	Leu	Phe	Leu	Lys	Met	Asp	His	Pro				
				165					170					175					
Glu	Asn	Trp	Asp	Ser	Pro	Tyr	Thr	Leu	His	Tyr	Thr	Glu	Tyr	Asp	Gly				
			180					185					190						
Lys	Thr	Gly	Ala	Thr	Gly	Thr	Lys	Lys	Thr	Met	Glu	Val	Asp	Ala	Val				
		195					200					205							
Ile	Gly	Ala	Asp	Gly	Ala	Asn	Ser	Arg	Val	Ala	Lys	Ser	Ile	Asp	Ala				
	210					215					220								
Gly	Asp	Tyr	Asp	Tyr	Ala	Ile	Ala	Phe	Gln	Glu	Arg	Ile	Arg	Ile	Pro				
225					230					235					240				
Asp	Glu	Lys	Met	Thr	Tyr	Tyr	Glu	Asp	Leu	Ala	Glu	Met	Tyr	Val	Gly				
				245					250					255					
Asp	Asp	Val	Ser	Pro	Asp	Phe	Tyr	Gly	Trp	Val	Phe	Pro	Lys	Cys	Asp				
			260					265					270						
His	Val	Ala	Val	Gly	Thr	Gly	Thr	Val	Thr	His	Lys	Gly	Asp	Ile	Lys				
		275					280					285							
Lys	Phe	Gln	Leu	Ala	Thr	Arg	Asn	Arg	Ala	Lys	Asp	Lys	Ile	Leu	Gly				
	290					295					300								
Gly	Lys	Ile	Ile	Arg	Val	Glu	Ala	His	Pro	Ile	Pro	Glu	His	Pro	Arg				
305					310					315					320				
Pro	Arg	Arg	Leu	Ser	Lys	Arg	Val	Ala	Leu	Val	Gly	Asp	Ala	Ala	Gly				
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Tyr	Val	Thr	Lys	Cys	Ser	Gly	Glu	Gly	Ile	Tyr	Phe	Ala	Ala	Lys	Ser				
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Gly	Arg	Met	Cys	Ala	Glu	Ala	Ile	Val	Glu	Gly	Ser	Gln	Asn	Gly	Lys				
		355					360					365							
Lys	Met	Ile	Asp	Glu	Gly	Asp	Leu	Arg	Lys	Tyr	Leu	Glu	Lys	Trp	Asp				
	370					375					380								
Lys	Thr	Tyr	Leu	Pro	Thr	Tyr	Arg	Val	Leu	Asp	Val	Leu	Gln	Lys	Val				
385					390					395					400				

Phe Tyr Arg Ser Asn Pro Ala Arg Glu Ala Phe Val Glu Met Cys Asn  
405 410 415

Asp Glu Tyr Val Gln Lys Met Thr Phe Asp Ser Tyr Leu Tyr Lys Arg  
420 425 430

Val Ala Pro Gly Ser Pro Leu Glu Asp Ile Lys Leu Ala Val Asn Thr  
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Ile Gly Ser Leu Val Arg Ala Asn Ala Leu Arg Arg Glu Ile Glu Lys  
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Leu Ser Val  
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<212> DNA
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<220>  
<223> PCR Primer

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32

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<210> 10
<211> 27
<212> DNA
<213> Artificial Sequence
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<220>  
<223> PCR Primer

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27

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<210> 11
<211> 27
<212> DNA
<213> Artificial Sequence
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<220>  
<223> PCR Primer

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27

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<212> DNA
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<220>  
<223> PCR Primer

<400> 12  
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<210> 13  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> PCR Primer

<400> 13  
 tctagattat gccagccagg ccttg 25

<210> 14  
 <211> 24  
 <212> DNA  
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<220>  
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<400> 14  
 ggatcctcca gcggacaagc caac 24

<210> 15  
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 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> PCR Primer

<400> 15  
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<210> 16  
 <211> 32  
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<220>  
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<400> 16  
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<210> 17  
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<220>  
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<400> 17  
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<210> 18  
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<220>  
 <223> PCR Primer

<400> 18  
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<210> 19  
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<220>  
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